

SEQUENCE LISTING

<110> Xu, Wenfeng
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 Lehner, Joyce M.
 Siadak, Anthony W.
 Sivakumar, Pallavur V.
 Moore, Margaret D.

<120> ANTI-IL-22RA ANTIBODIES AND BINDING
 PARTNERS AND METHODS OF USING IN INFLAMMATION

<130> 03-02

<150> US 60/457,481
 <151> 2003-03-24

<150> US 60/523,295
 <151> 2003-11-17

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 Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
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ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150
 Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
 25 30 35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc 198
 Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
 40 45 50 55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt 246
 Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
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cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac 294
 Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
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ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc 342

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Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
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acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	atc	tcc	aaa	gtg	aga	tcg	att	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
120						125				130					135	
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Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
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His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
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Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
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aga	gaa	tat	gag	ttc	ttc	ggc	ctg	acc	cct	gac	aca	gag	ttc	ctt	ggc	630
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acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	gcc	aag	gag	agt	gcc	ccc	tac	678
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Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
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Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
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Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
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Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
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Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
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Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	
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Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	
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Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	
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Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
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Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
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Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
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His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
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Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
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Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
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 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
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 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
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 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
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 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
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 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
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 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
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 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 370 375 380
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400

Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
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 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
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 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
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 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
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 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
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 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
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 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
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 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
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 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
 115 120 125
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 130 135 140
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
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 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
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 Thr Trp Thr
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<223> A Soluble IL-22RA-Fc Fusion Polypeptide

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 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
 115 120 125
 Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
 130 135 140
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
 145 150 155 160
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 165 170 175
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
 180 185 190
 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
 195 200 205
 Thr Trp Thr Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
 210 215 220
 Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 225 230 235 240
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
 245 250 255
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
 260 265 270
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 275 280 285
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 290 295 300
 Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 305 310 315 320
 Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 325 330 335
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 340 345 350
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 355 360 365
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 370 375 380
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 385 390 395 400
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
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 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
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 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
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 Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 450 455 460
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
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 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

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 Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
 15 20 25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac	149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp	
30 35 40	

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg	197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu	
45 50 55	

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atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa      341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
         95          100          105

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 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
 110 115 120

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agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg      437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125          130          135

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cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt      485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140                      145                      150                      155

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 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
Met Ser Leu Arg Asn Ala Cys Ile
175

taacccccc ttccctgctag aaataacaat tagatgcccc aaagcgattt ttttaacca 647

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catagatatt	tattgataac	atttcatgt	aactgggttt	ctatacacag	aaaacaattt	827
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aaacccctaa	atagcttcat	gtttccataa	tcagtacttt	atatttataa	atgtattttat	947
tattattata	agactgcatt	ttatttataat	cattttatta	atatggattt	attatagaa	1007
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	Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln	35	40	45		
	Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser	50	55	60		
	Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe	65	70	75	80	
	His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu	85	90	95		
	Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln	100	105	110		
	Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg	115	120	125		
	Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn	130	135	140		
	Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu	145	150	155	160	
	Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn	165	170	175		
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Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr	5	10	15	20		
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Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile Ala	25	30	35			

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Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa Ile Arg Gly Ser	
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gtg caa gcc aaa gat gga aac att gac atc aga atc tta agg agg act	248
Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu Arg Arg Thr	
55 60 65	
gag tct ttg caa gac aca aag cct gcg aat cga tgc tgc ctc ctg cgc	296
Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys Cys Leu Leu Arg	
70 75 80	
cat ttg cta aga ctc tat ctg gac agg gta ttt aaa aac tac cag acc	344
His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys Asn Tyr Gln Thr	
85 90 95 100	
cct gac cat tat act ctc cgg aag atc agc agc ctc gcc aat tcc ttt	392
Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu Ala Asn Ser Phe	
105 110 115	
ctt acc atc aag aag gac ctc cgg ctc tgt cat gcc cac atg aca tgc	440
Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala His Met Thr Cys	
120 125 130	
cat tgt ggg gag gaa gca atg aag aaa tac agc cag att ctg agt cac	488
His Cys Gly Glu Glu Ala Met Lys Lys Tyr Ser Gln Ile Leu Ser His	
135 140 145	
ttt gaa aag ctg gaa cct cag gca gca gtt gtg aag gct ttg ggg gaa	536
Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys Ala Leu Gly Glu	
150 155 160	
cta gac att ctt ctg caa tgg atg gag gag aca gaa tag gagaaaagtg	585
Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu *	
165 170 175	
atgctgctgc taagaatatt cgaggtcaag agtccagtc ttcaataacct gcagaggagg	645
catgacccca aaccaccatc tctttactgt actagtcttg tgctggtcac agtgtatctt	705
atttatgcat tacttgcttc cttgcattgt tgcattttatg catcccaat cttatttgag	765
accatacttg tataagattt ttgtatatac ttctgtat tggatatatt tattatgttt	825
tatattttat tatttttgc tattaatgtt ttatatttt tacttggca tgaaacttta	885
aaaaaaattc acaagattat atttataacc tgactagagc a	926
<210> 8	
<211> 176	
<212> PRT	
<213> Homo sapiens	
<220>	
<221> VARIANT	
<222> (48)...(48)	
<223> Amino acid at position 48 can be a D (Asp) or E (Glu)	
<221> VARIANT	
<222> 48	
<223> Xaa = Any Amino Acid	
<400> 8	
Met Lys Ala Ser Ser Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr	
1 5 10 15	
Leu Leu Trp Thr Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser	
20 25 30	
Cys Val Ile Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Xaa	
35 40 45	

Ile Arg Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile
 50 55 60
 Leu Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 65 70 75 80
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe Lys
 85 90 95
 Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110
 Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu Cys His Ala
 115 120 125
 His Met Thr Cys His Cys Gly Glu Ala Met Lys Lys Tyr Ser Gln
 130 135 140
 Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln Ala Ala Val Val Lys
 145 150 155 160
 Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln Trp Met Glu Glu Thr Glu
 165 170 175

<210> 9
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide Linker

<400> 9
 Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10 15

<210> 10
 <211> 1050
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (5)...(589)

<400> 10
 aaca ggc tct cct ctc act tat caa ctt ttg aca ctt gtg cga tcg gtg 49
 Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val
 1 5 10 15

atg gct gtc ctg cag aaa tct atg agt ttt tcc ctt atg ggg act ttg 97
 Met Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu
 20 25 30

gcc gcc agc tgc ctg ctt ctc att gcc ctg tgg gcc cag gag gca aat 145
 Ala Ala Ser Cys Leu Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn
 35 40 45

gcg ctg ccc atc aac acc cgg tgc aag ctt gag gtg tcc aac ttc cag 193
 Ala Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln
 50 55 60

cag ccg tac atc gtc aac cgc acc ttt atg ctg gcc aag gag gcc agc 241
 Gln Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 65 70 75

ctt gca gat aac aac aca gac gtc cgg ctc atc ggg gag aaa ctg ttc 289
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 80 85 90 95

cga gga gtc agt gct aag gat cag tgc tac ctg atg aag cag gtg ctc 337

Arg Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu			
100	105	110	
aac ttc acc ctg gaa gac att ctg ctc ccc cag tca gac agg ttc cg			385
Asn Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg			
115	120	125	
ccc tac atg cag gag gtg gtg cct ttc ctg acc aaa ctc agc aat cag			433
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln			
130	135	140	
ctc agc tcc tgt cac atc agt ggt gac gac cag aac atc cag aag aat			481
Leu Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn			
145	150	155	
gtc aga agg ctg aag gag aca gtg aaa aag ctt gga gag agc gga gag			529
Val Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu			
160	165	170	175
atc aaa gcg atc ggg gaa ctg gac ctg ctg ttt atg tct ctg aga aat			577
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn			
180	185	190	
gct tgc gtc tga gcgagaagaa gctagaaaaac gaagaactgc tccttcctgc			629
Ala Cys Val *			

cttctaaaaa gaacaataag atccctgaat ggactttttt actaaaggaa agtggagaagc			689
taacgtccac catcattaga agatttcaca tgaacacctgg ctcagtgaa agagaaaata			749
gtgtcaagtt gtccatgaga ccagaggttag acttgataac cacaagatt cattgacaat			809
attttattgt cattgataat gcaacagaaa aagttatgtac tttaaaaaat tgtttgaag			869
gagggttacct ctcatttcctc tagaagaaaa gcctatgtaa cttcatttcc ataaccaata			929
ctttatataat gtaagttat ttattataag tatacatttt attttagtca gtttattaat			989
atggattttat ttatagaaaa attatctgtat gttgatattt gagtataaag caaataataat			1049
t			1050

<210> 11
<211> 194
<212> PRT
<213> Mus musculus

<400> 11			
Gly Ser Pro Leu Thr Tyr Gln Leu Leu Thr Leu Val Arg Ser Val Met			
1 5 10 15			
Ala Val Leu Gln Lys Ser Met Ser Phe Ser Leu Met Gly Thr Leu Ala			
20 25 30			
Ala Ser Cys Leu Leu Ile Ala Leu Trp Ala Gln Glu Ala Asn Ala			
35 40 45			
Leu Pro Ile Asn Thr Arg Cys Lys Leu Glu Val Ser Asn Phe Gln Gln			
50 55 60			
Pro Tyr Ile Val Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser Leu			
65 70 75 80			
Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe Arg			
85 90 95			
Gly Val Ser Ala Lys Asp Gln Cys Tyr Leu Met Lys Gln Val Leu Asn			
100 105 110			
Phe Thr Leu Glu Asp Ile Leu Leu Pro Gln Ser Asp Arg Phe Arg Pro			
115 120 125			
Tyr Met Gln Glu Val Val Pro Phe Leu Thr Lys Leu Ser Asn Gln Leu			
130 135 140			
Ser Ser Cys His Ile Ser Gly Asp Asp Gln Asn Ile Gln Lys Asn Val			
145 150 155 160			
Arg Arg Leu Lys Glu Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile			
165 170 175			
Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala			
180 185 190			

Cys Val

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<210> 12
<211> 2149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(693)

<400> 12
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Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
1 5 10 15

act ggt gta gca gga act cag tca acg cat gag tct ctg aag cct cag 96
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln
20 25 30

agg gta caa ttt cag tcc cga aat ttt cac aac att ttg caa tgg cag 144
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln
35 40 45

cct ggg agg gca ctt act ggc aac agc agt gtc tat ttt gtg cag tac 192
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr
50 55 60

aaa ata tat gga cag aga caa tgg aaa aat aaa gaa gac tgt tgg ggt 240
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly
65 70 75 80

act caa gaa ctc tct tgt gac ctt acc agt gaa acc tca gac ata cag 288
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln
85 90 95

gaa cct tat tac ggg agg gtg agg gcg gcc tcg gct ggg agc tac tca 336
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser
100 105 110

gaa tgg agc atg acg ccg cgg ttc act ccc tgg tgg gaa aca aaa ata 384
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile
115 120 125

gat cct cca gtc atg aat ata acc caa gtc aat ggc tct ttg ttg gta 432
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val
130 135 140

att ctc cat gct cca aat tta cca tat aga tac caa aag gaa aaa aat 480
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn
145 150 155 160

gta tct ata gaa gat tac tat gaa cta cta tac cga gtt ttt ata att 528
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile
165 170 175

aac aat tca cta gaa aag gag caa aag gtt tat gaa ggg gct cac aga 576
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg
180 185 190

gcg gtt gaa att gaa gct cta aca cca cac tcc agc tac tgt gta gtg 624
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val
195 200 205

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gct gaa ata tat cag ccc atg tta gac aga aga agt cag aga agt gaa	672
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	
210 215 220	
gag aga tgt gtg gaa att cca tgacttgtgg aatttggcat tcagcaatgt	723
Glu Arg Cys Val Glu Ile Pro	
225 230	
ggaaaattcta aagctccctg agaacaggat gactcgtgtt tgaaggatct tatttaaat	783
tgttttcta ttttctaaa gcaatattca ctgttacacc ttggggactt ctttgtttat	843
ccattcttt atcctttata tttcatttta aactatattt gaacgcatt ccccccggaaa	903
aattgaaatg taaagatgag gcagagaata aagtgttcta taaaatctag aactttattt	963
ctgaatgtaa catccctaata aacaacccctc attcttctaa tacagcaaaa taaaatcttta	1023
acaaccaagg aatagtattt aagaaaatgt taaaataattt tttttaaat agcattacag	1083
actgaggcgg tcctgaagca atgggttttca actctcttat tgagccaatt aaattgacat	1143
tgccttgaca atttaaaaact tctataaagg taaaatattt tcatacattt ctatattata	1203
tgaatataact ttatattat taaaatattt tacttaatga atcaaaaattt	1263
tgtttttaag tctactttat gtaaataaga acaggttttggggaaaaaaa tctttagatt	1323
tctggattga tatctgaattt aaaaatctca aacaacaaagg agtctacttcttgcataattgt	1383
ccctcattta aaagataatat taagctttc tttctgtttt gttttgttt ttttagttt	1443
ttaatcctgt cttagaagaa cttatctta ttctcaaaaat taaaatgtaat ttttttagtg	1503
acaaaagaaga aaggaaaacctt cattactcaa tccttctggc caagagtgtc ttgcttgcgg	1563
cgccttcctc atctctat aggaggatcc catgaatgtat gtttattgg gaactgctgg	1623
ggtcgaccccc atacagagaa ctcagcttga agcttggaaagc acacagtgg tagcaggaga	1683
aggaccgggtt ttggtaggtg cttacagaga ctatagagct agacaaagcc ctccaaactg	1743
gccccttcctg ctcactgcctt ctcctgagta gaaatctggt gacctaaggc tcagtgcgg	1803
caacagaaaag ctgccttcctt cacttgaggc taagtcttca tatatgttttta aggttgcctt	1863
tcttagtggg agatacatat cagagaacat ttgtacaattt ccccatgaaa attgctccaa	1923
agttgataac aatatagtcg gtgcttcttag ttatatgcaa gtactcaatg ataaatggat	1983
taaaaaatat tcagaaaatgt attgggggggt ggaggagaat aagaggcaga gcaagagcta	2043
gagaattgggt ttccttgctt ccctgtatgc tcagaaaaca ttgattttag catagacgca	2103
gagactgaaa aaaaaaaaaat gctcgagcgg ccggccatatc ctgggt	2149
<210> 13	
<211> 231	
<212> PRT	
<213> Homo sapiens	
<400> 13	
Met Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu	
1 5 10 15	
Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro Gln	
20 25 30	
Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln Trp Gln	
35 40 45	
Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe Val Gln Tyr	
50 55 60	
Lys Ile Tyr Gly Gln Arg Gln Trp Lys Asn Lys Glu Asp Cys Trp Gly	
65 70 75 80	
Thr Gln Glu Leu Ser Cys Asp Leu Thr Ser Glu Thr Ser Asp Ile Gln	
85 90 95	
Glu Pro Tyr Tyr Gly Arg Val Arg Ala Ala Ser Ala Gly Ser Tyr Ser	
100 105 110	
Glu Trp Ser Met Thr Pro Arg Phe Thr Pro Trp Trp Glu Thr Lys Ile	
115 120 125	
Asp Pro Pro Val Met Asn Ile Thr Gln Val Asn Gly Ser Leu Leu Val	
130 135 140	
Ile Leu His Ala Pro Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn	
145 150 155 160	
Val Ser Ile Glu Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile	
165 170 175	
Asn Asn Ser Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg	
180 185 190	
Ala Val Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val	
195 200 205	
Ala Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu	

210 Glu Arg Cys Val Glu Ile Pro 225	215 230	220	
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<210> 14
<211> 699
<212> DNA
<213> Artificial Sequence

<220>
<223> C-Terminal Fc4 tag

<400> 14
gagcccatat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag      60
ggggcaccgt cagtcttcct cttcccccctt aaacccaagg acaccctcat gatctcccg      120
acccttgggg tcacatgcgt ggtgggtggac gtgagccacg aagaccctga ggtcaagttc      180
aactggtacg tggacggcgt ggaggtgcatt aatgccaaga caaagccgcg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
ggcaaggagt acaagtgcac ggtctccaaac aaagccctcc catcctccat cgagaaaacc      360
atctccaaag ccaaaggcgt gccccgagaa ccacagggtgt acaccctgccc cccatcccg      420
gatgagctga ccaagaacca ggtcagcgtt acctgcctgg tcaaaggctt ctatcccagc      480
gacatcgccc tggagtggaa gagcaatggg cagccggaga acaactacaa gaccacgcct      540
cccggtctgg actccgacgg ctccttcctt ctctacagca agtcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
tacacgcaga agaggctctc cctgtctccg ggtaaataaa      699

<210> 15
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Peptide Tag

<400> 15
Glu Tyr Met Pro Met Glu
 1           5

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu (CEE) Peptide Tag with spacer

<400> 16
Gly Ser Gly Gly Glu Tyr Met Pro Met Glu
 1           5           10

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39289

<400> 17
tccgaggagt caatgcttaag
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20

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<210> 18
<211> 20

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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39290

<400> 18
tccaagctt ttcactgtct 20

<210> 19
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39776

<400> 19
gggccccgcta gcacct 16

<210> 20
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer ZC39777

<400> 20
gggtgatccg ctggca 16

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-20 FAM/TAMRA labeled TaqMan probe ZC38752

<400> 21
ccagccactt tctctctccg tatttcttat attcca 36

<210> 22
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer, ZC42459

<400> 22
tggccaggct cagcaa 16

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer, ZC42458

<400> 23
gcacattcct ctggatatgc a 21

<210> 24
<211> 31

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<212> DNA			
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<220>			
<223> IL-22 TaqMan probe, ZC42460			
<400> 24			
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<210> 25			
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<220>			
<223> forward primer, ZC40541			
<400> 25			
tgcgccaattc ctttcttacc a			21
<210> 26			
<211> 20			
<212> DNA			
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<220>			
<223> reverse primer, ZC40542			
<400> 26			
cccacacaatgg catgtcatgt			20
<210> 27			
<211> 25			
<212> DNA			
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<220>			
<223> IL-20 TaqMan® probe ZC40544			
<400> 27			
agaaggacct ccggctctgt catgc			25
<210> 28			
<211> 57			
<212> DNA			
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<220>			
<223> Oligonucleotide primer ZC45,593			
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caggaaatcc atgccgagtt gagacgcttc cgttagacacg cccctgagga cccctcg			57
<210> 29			
<211> 63			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Oligonucleotide primer ZC45,592			
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ctt			63
<210> 30			

<211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC45,591

 <400> 30
 gaccggacag gaagcgggtc tggaagcggg tctggaagcg gtgagccag aggccccaca 60
 atc 63

 <210> 31
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide primer ZC45,594

 <400> 31
 agagctgttt taaggcgcbc ctcttagatta tttttatata cccggagtcc gggagaa 57

 <210> 32
 <211> 531
 <212> DNA
 <213> Mus musculus

 <220>
 <221> CDS
 <222> (1)...(531)

 <400> 32
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 Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe
 1 5 10 15

 ctt ctc tgg act cct tta act ggg ctc aag acc ctc cat ttg gga agc 96
 Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser
 20 25 30

 tgt gtg att act gca aac cta cag gca ata caa aag gaa ttt tct gag 144
 Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu
 35 40 45

 att cgg gat agt gtg caa gct gaa gat aca aat att gac atc aga att 192
 Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile
 50 55 60

 tta agg acg act gag tct ttg aaa gac ata aag tct ttg gat agg tgc 240
 Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys
 65 70 75 80

 tgc ttc ctt cgt cat cta gtg aga ttc tat ctg gac agg gta ttc aaa 288
 Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys
 85 90 95

 gtc tac cag acc cct gac cac cat acc ctg aga aag atc agc agc ctc 336
 Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu
 100 105 110

 gcc aac tcc ttt ctt atc atc aag aag gac ctc tca gtc tgt cat tct 384
 Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser
 115 120 125

 cac atg gca tgt cat tgt ggg gaa gaa gca atg gag aaa tac aac caa 432
 His Met Ala Cys His Cys Gly Glu Ala Met Glu Lys Tyr Asn Gln

130

135

140

att ctg agt cac ttc ata gag ttg gaa ctt cag qca qcg gtg gta aag	480
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys	
145 150 155 160	
gct ttg gga gaa cta ggc att ctt ctg aga tgg atg gag gag atg cta	528
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu	
165 170 175	
tag	531
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<210> 33
<211> 176
<212> PRT
<213> Mus musculus

<400> 33

Met Lys Gly Phe Gly Leu Ala Phe Gly Leu Phe Ser Ala Val Gly Phe	
1 5 10 15	
Leu Leu Trp Thr Pro Leu Thr Gly Leu Lys Thr Leu His Leu Gly Ser	
20 25 30	
Cys Val Ile Thr Ala Asn Leu Gln Ala Ile Gln Lys Glu Phe Ser Glu	
35 40 45	
Ile Arg Asp Ser Val Gln Ala Glu Asp Thr Asn Ile Asp Ile Arg Ile	
50 55 60	
Leu Arg Thr Thr Glu Ser Leu Lys Asp Ile Lys Ser Leu Asp Arg Cys	
65 70 75 80	
Cys Phe Leu Arg His Leu Val Arg Phe Tyr Leu Asp Arg Val Phe Lys	
85 90 95	
Val Tyr Gln Thr Pro Asp His His Thr Leu Arg Lys Ile Ser Ser Leu	
100 105 110	
Ala Asn Ser Phe Leu Ile Ile Lys Lys Asp Leu Ser Val Cys His Ser	
115 120 125	
His Met Ala Cys His Cys Gly Glu Glu Ala Met Glu Lys Tyr Asn Gln	
130 135 140	
Ile Leu Ser His Phe Ile Glu Leu Glu Leu Gln Ala Ala Val Val Lys	
145 150 155 160	
Ala Leu Gly Glu Leu Gly Ile Leu Leu Arg Trp Met Glu Glu Met Leu	
165 170 175	

<210> 34
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC22901

<400> 34
catcaaaccg cctgatgtga c

21

<210> 35
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC45039

<400> 35
attaggcttg ggaggaaatg g

21

<210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC38573

<400> 36
 tggcgatgcc tgcttgccga ata 23

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC25223

<400> 37
 gtttccctca catctgttat cg 22

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC40128

<400> 38
 ggcttgaact ttgagaaaagg cagt 24

<210> 39
 <211> 1473
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IL-22RA Extracellular domain with tPA leader and
 fused to murine gamma 2a heavy chain Fc region
 (mG2a)

<221> CDS
 <222> (1)...(1473)

<400> 39
 atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt ggc 48
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gcc gtc ttc gtt tcg ctc agc cag gaa atc cat gcc gag ttg aga cgc 96
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
 20 25 30

ttc cgt aga cac gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg 144
 Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
 35 40 45

aaa ttc cag tcc agc aac ttt gaa aac atc ctg acg tgg gac agc ggg 192
 Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
 50 55 60

cca gag ggc acc cca gac acg gtc tac agc atc gag tat aag acg tac 240
 Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr

65	70	75	80	
gga gag agg gac tag gtg gca aag aag ggc tgt cag cgg atc acc acc cg				288
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg				
85	90	95		
aag tcc tgc aac ctg acg gtg gag acg ggc aac ctc acg gag ctc tac				336
Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr				
100	105	110		
tat gcc agg gtc acc gct gtc agt gcg gga ggc cgg tca gcc acc aag				384
Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys				
115	120	125		
atg act gac agg ttc agc tct ctg cag cac act acc ctc aag cca cct				432
Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro				
130	135	140		
gat gtg acc tgt atc tcc aaa gtg aga tcg att cag atg att gtt cat				480
Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His				
145	150	155	160	
cct acc ccc acg cca atc cgt gca ggc gat ggc cac cgg cta acc ctg				528
Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu				
165	170	175		
gaa gac atc ttc cat gac ctg ttc tac cac tta gag ctc cag gtc aac				576
Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn				
180	185	190		
cgc acc tac caa atg cac ctt gga ggg aag cag aga gaa tat gag ttc				624
Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe				
195	200	205		
ttc ggc ctg acc cct gac aca gag ttc ctt ggc acc atc atg att tgc				672
Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys				
210	215	220		
gtt ccc acc tgg gcc aag gag agt gcc ccc tac atg tgc cga gtg aag				720
Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys				
225	230	235	240	
aca ctg cca gac cgg aca gga agc ggg tct gga agc ggg tct gga agc				768
Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser				
245	250	255		
ggt gag ccc aga ggc ccc aca atc aag ccc tgt cct cca tgc aaa tgc				816
Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys				
260	265	270		
cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca				864
Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro				
275	280	285		
aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt				912
Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys				
290	295	300		
gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg				960
Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp				
305	310	315	320	
ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga				1008
Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg				
325	330	335		

gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag	1056		
Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln			
340	345	350	
cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac	1104		
His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn			
355	360	365	
aaa gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg	1152		
Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly			
370	375	380	
tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag	1200		
Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu			
385	390	395	400
atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg	1248		
Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met			
405	410	415	
cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta	1296		
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu			
420	425	430	
aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc	1344		
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe			
435	440	445	
atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat	1392		
Met Tyr Ser Lys Leu Arg Val Glu Lys Asn Trp Val Glu Arg Asn			
450	455	460	
agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg	1440		
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr			
465	470	475	480
act aag agc ttc tcc cgg act ccg ggt aaa taa	1473		
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys *			
485	490		

<210> 40
<211> 490
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-22RA Extracellular domain with tPA leader and
fused to murine gamma 2a heavy chain Fc region
(mG2a)

<400> 40
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg
20 25 30
Phe Arg Arg His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val
35 40 45
Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly
50 55 60
Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr
65 70 75 80
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg
85 90 95
Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr
100 105 110

Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys
 115 120 125
 Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro
 130 135 140
 Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His
 145 150 155 160
 Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu
 165 170 175
 Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn
 180 185 190
 Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe
 195 200 205
 Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys
 210 215 220
 Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys
 225 230 235 240
 Thr Leu Pro Asp Arg Thr Gly Ser Gly Ser Gly Ser Gly Ser
 245 250 255
 Gly Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
 260 265 270
 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
 275 280 285
 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
 290 295 300
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
 305 310 315 320
 Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
 325 330 335
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
 340 345 350
 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 355 360 365
 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
 370 375 380
 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
 385 390 395 400
 Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
 405 410 415
 Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
 420 425 430
 Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
 435 440 445
 Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
 450 455 460
 Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
 465 470 475 480
 Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
 485 490

<210> 41
 <211> 1834
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (43)...(1788)

<400> 41
 ttgggtccaga gccgaggccc gaagggggcc tggagggacc ca atg aag aca cta 54
 Met Lys Thr Leu
 1

ctg acc atc ctg acg gtg gga tcc ctg gcc gct cac acc act gtg gac 102
 Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His Thr Thr Val Asp

5	10	15	20	
aca tcc ggt ctc ctt caa cac gtg aaa ttc cag tcc agc aac ttt gag				150
Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu				
25	30		35	
aac atc ttg acg tgg gat ggt ggg ccc gct agc acc tct gac acc gtc				198
Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr Ser Asp Thr Val				
40	45		50	
tac agt gtg gaa tat aag aaa tac gga gag aga aag tgg ctg gcc aag				246
Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys Trp Leu Ala Lys				
55	60		65	
gcg ggc tgc cag cgg atc acc cag aag ttc tgc aac ctg act atg gag				294
Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys Asn Leu Thr Met Glu				
70	75		80	
acc cgc aac cac act gag ttt tac tac gcc aag gtc acg gca gtc agc				342
Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val Ser				
85	90		95	100
gca gga ggc cca cca gtc aca aag atg act gat cgt ttc agc tcg ctg				390
Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp Arg Phe Ser Ser Leu				
105	110		115	
cag cac act acc atc aaa ccg cct gat gtg acc tgc atc ccc aaa gtg				438
Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr Cys Ile Pro Lys Val				
120	125		130	
agg tcc att cag atg ctg gtc cac ccc aca ctc aca ccg gtc ctc tcg				486
Arg Ser Ile Gln Met Leu Val His Pro Thr Leu Thr Pro Val Leu Ser				
135	140		145	
gaa gat ggc cac cag cta acc ctg gag gag att ttc cat gac ctg ttc				534
Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe				
150	155		160	
tac cgc tta gag ctc cac gtc aac cac acc tac cag atg cac ctt gaa				582
Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr Gln Met His Leu Glu				
165	170		175	180
ggc aaa cag aga gaa tac gag ttc ctt ggc ctg act ccc gac aca gag				630
Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro Asp Thr Glu				
185	190		195	
ttc ctc ggc tcc atc aca att ttg act ccg ata ttg tcc aag gaa agt				678
Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser Lys Glu Ser				
200	205		210	
gcc ccc tac gtg tgc cga gtg aag acg ctg ccc gat cgg acg tgg gcc				726
Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Ala				
215	220		225	
tac tcc ttc tcg ggc gcc gtg ctc ttt tcc atg ggt ttc ctc gtc ggc				774
Tyr Ser Phe Ser Gly Ala Val Leu Phe Ser Met Gly Phe Leu Val Gly				
230	235		240	
ttg ctc tgt tat ctg ggc tac aaa tac atc acc aag cca cct gta cct				822
Leu Leu Cys Tyr Leu Gly Tyr Lys Tyr Ile Thr Lys Pro Pro Val Pro				
245	250		255	260
cct aac tcc ctg aac gtc caa cgt gtc ctg acc ttt caa ccc cta cgc				870
Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg				
265	270		275	

ttc atc caa gaa cac gta ctg atc cct gtc ttg gac ctc agt ggc ccc	918
Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp Leu Ser Gly Pro	
280 285 290	
agc agt ctg cct cag ccc atc cag tac tcc caa gtg gtg gtg tct ggg	966
Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val Val Val Ser Gly	
295 300 305	
ccc agg gag cct cct gga gct gtg tgg cgg cag agc ctg tct gac ctc	1014
Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser Leu Ser Asp Leu	
310 315 320	
acc tac gta ggg cag tca gat gtc tcc atc ctg caa cct acc aac gtg	1062
Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln Pro Thr Asn Val	
325 330 335 340	
cca gct cag cag aca ctg tcc cca cca tcc tac gct ccg aag gct gtc	1110
Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala Pro Lys Ala Val	
345 350 355	
cct gag gtc cag ccc cct tcc tat gcg cct cag gta gcc tcg gat gcc	1158
Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val Ala Ser Asp Ala	
360 365 370	
aaa gct ctg ttc tac tca cca caa cag ggg atg aag acc agg cct gcc	1206
Lys Ala Leu Phe Tyr Ser Pro Gln Gln Gly Met Lys Thr Arg Pro Ala	
375 380 385	
acc tat gac ccg cag gac att ctg gac agc tgc cct gct tct tat gct	1254
Thr Tyr Asp Pro Gln Asp Ile Leu Asp Ser Cys Pro Ala Ser Tyr Ala	
390 395 400	
gtg tgt gtg gaa gac tct ggc aaa gac tct acc cca ggc atc ctc tcc	1302
Val Cys Val Glu Asp Ser Gly Lys Asp Ser Thr Pro Gly Ile Leu Ser	
405 410 415 420	
act ccc aaa tac ctc aag aca aaa ggt cag ctc cag gaa gac aca ctt	1350
Thr Pro Lys Tyr Leu Lys Thr Lys Gly Gln Leu Gln Glu Asp Thr Leu	
425 430 435	
gtt aga agc tgt ctc cca ggg gac ctt tct cta cag aaa gtc acc tcc	1398
Val Arg Ser Cys Leu Pro Gly Asp Leu Ser Leu Gln Lys Val Thr Ser	
440 445 450	
tta ggt gaa ggg gag aca cag aga cca aaa tca ctc ccc tca cct ctg	1446
Leu Gly Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu Pro Ser Pro Leu	
455 460 465	
gga ttt tgc aca gac aga gga cct gac ctt cac aca ctg cgc agt gag	1494
Gly Phe Cys Thr Asp Arg Gly Pro Asp Leu His Thr Leu Arg Ser Glu	
470 475 480	
gaa cca gag aca cca cgg tac ctg aag ggg gcg ctg tct ctc ctg tcc	1542
Glu Pro Glu Thr Pro Arg Tyr Leu Lys Gly Ala Leu Ser Leu Leu Ser	
485 490 495 500	
tct gtg cag atc gag ggc cac cct gtc tcc ctc cct ttg cac gtc cat	1590
Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro Leu His Val His	
505 510 515	
tct gtc tca tgt tcc ccc tca gac gag gga cca agt ccc tgg ggc ctg	1638
Ser Val Ser Cys Ser Pro Ser Asp Glu Gly Pro Ser Pro Trp Gly Leu	
520 525 530	
ctg gac tcc ctt gtg tgt cca aag gat gag ggt ccc gcg gtt gag act	1686
Leu Asp Ser Leu Val Cys Pro Lys Asp Glu Gly Pro Ala Val Glu Thr	

535	540	545	
gag gcc atg tgc ccc agt gct gca gcc tct gag ctg gag cag tcc aca			1734
Glu Ala Met Cys Pro Ser Ala Ala Ala Ser Glu Leu Glu Gln Ser Thr			
550 555 560			
gaa ctg gac tct ctt ttc aaa ggc ttg gcc ctg act gtg cag tgg gaa			1782
Glu Leu Asp Ser Leu Phe Lys Gly Leu Ala Leu Thr Val Gln Trp Glu			
565 570 575 580			
tcc tga agggagatcg gagcaagcag gcctaagttt cctcccgccc caccta			1834
Ser *			

<210> 42
 <211> 581
 <212> PRT
 <213> Mus musculus

<400> 42
 Met Lys Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15
 Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser Thr
 35 40 45
 Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg Lys
 50 55 60
 Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys Asn
 65 70 75 80
 Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Pro Lys Val Arg Ser Ile Gln Met Leu Val His Pro Thr Leu Thr
 130 135 140
 Pro Val Leu Ser Glu Asp Gly His Gln Leu Thr Leu Glu Glu Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr Arg Leu Glu Leu His Val Asn His Thr Tyr Gln
 165 170 175
 Met His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu
 195 200 205
 Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Ala Tyr Ser Phe Ser Gly Ala Val Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Gly Leu Leu Cys Tyr Leu Gly Tyr Lys Tyr Ile Thr Lys
 245 250 255
 Pro Pro Val Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 260 265 270
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Leu Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Pro Gln Pro Ile Gln Tyr Ser Gln Val
 290 295 300
 Val Val Ser Gly Pro Arg Glu Pro Pro Gly Ala Val Trp Arg Gln Ser
 305 310 315 320
 Leu Ser Asp Leu Thr Tyr Val Gly Gln Ser Asp Val Ser Ile Leu Gln
 325 330 335
 Pro Thr Asn Val Pro Ala Gln Gln Thr Leu Ser Pro Pro Ser Tyr Ala
 340 345 350
 Pro Lys Ala Val Pro Glu Val Gln Pro Pro Ser Tyr Ala Pro Gln Val

355	360	365	
Ala Ser Asp Ala Lys Ala	Leu Phe Tyr Ser Pro Gln	Gln Gly Met Lys	
370	375	380	
Thr Arg Pro Ala Thr Tyr Asp	Pro Gln Asp Ile Leu Asp Ser Cys Pro		
385	390	395	400
Ala Ser Tyr Ala Val Cys Val Glu Asp	Ser Gly Lys Asp Ser Thr Pro		
405	410		415
Gly Ile Leu Ser Thr Pro Lys Tyr	Leu Lys Thr Lys Gly Gln Leu Gln		
420	425	430	
Glu Asp Thr Leu Val Arg Ser	Cys Leu Pro Gly Asp Leu Ser Leu Gln		
435	440	445	
Lys Val Thr Ser Leu Gly	Glu Gly Glu Thr Gln Arg Pro Lys Ser Leu		
450	455	460	
Pro Ser Pro Leu Gly Phe Cys Thr Asp Arg	Gly Pro Asp Leu His Thr		
465	470	475	480
Leu Arg Ser Glu Glu Pro Glu Thr Pro Arg	Tyr Leu Lys Gly Ala Leu		
485	490		495
Ser Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Val Ser Leu Pro			
500	505	510	
Leu His Val His Ser Val Ser Cys Ser Pro Ser Asp	Glu Gly Pro Ser		
515	520	525	
Pro Trp Gly Leu Leu Asp Ser	Leu Val Cys Pro Lys Asp Glu Gly Pro		
530	535	540	
Ala Val Glu Thr Glu Ala Met Cys Pro Ser	Ala Ala Ala Ser Glu Leu		
545	550	555	560
Glu Gln Ser Thr Glu Leu Asp Ser Leu	Phe Lys Gly Leu Ala Leu Thr		
565	570		575
Val Gln Trp Glu Ser			
580			

<210> 43
<211> 660
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (1) . . . (660)

<400> 43	atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca	48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser		
1 5 10 15		
gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	96	
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val		
20 25 30		
aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	144	
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly		
35 40 45		
aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	192	
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp		
50 55 60		
aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	240	
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser		
65 70 75 80		
aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	288	
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu		
85 90 95		
cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	336	

His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105						110		
att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120						125			
atg	cgt	ttc	tta	gcc	cct	aaa	att	gag	aat	gaa	tac	gaa	act	tgg	act	432
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	
		130				135					140					
atg	aag	aat	gtg	tat	aac	tca	tgg	act	tat	aat	gtg	caa	tac	tgg	aaa	480
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	
		145				150				155			160			
aac	ggg	act	gat	gaa	aag	ttt	caa	att	act	ccc	cag	tat	gac	ttt	gag	528
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	
			165				170						175			
gtc	ctc	aga	aac	ctg	gag	cca	tgg	aca	act	tat	tgt	gtt	caa	gtt	cga	576
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	
			180				185						190			
ggg	ttt	ctt	cct	gat	cgg	aac	aaa	gct	ggg	gaa	tgg	agt	gag	cct	gtc	624
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	
		195				200						205				
tgt	gag	caa	aca	acc	cat	gac	gaa	acg	gtc	ccc	tcc					660
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser					
		210				215					220					

<210> 44
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 44
 Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 45
 <211> 199
 <212> PRT
 <213> homo sapiens

<400> 45
 Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
 1 5 10 15
 Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
 20 25 30
 Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
 35 40 45
 Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
 50 55 60
 Asp His Thr Leu Arg Val Ala Glu Phe Ala Asp Glu His Ser Asp
 65 70 75 80
 Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
 85 90 95
 Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
 100 105 110
 Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
 115 120 125
 Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
 130 135 140
 Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
 145 150 155 160
 Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
 165 170 175
 Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
 180 185 190
 Thr Thr His Asp Glu Thr Val
 195

<210> 46
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 46
 Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
 1 5 10 15
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
 20 25 30
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
 35 40 45
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
 50 55 60
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
 65 70 75 80
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
 85 90 95
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
 100 105 110
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
 115 120 125
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
 130 135 140
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
 145 150 155 160
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
 165 170 175
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
 180 185 190

Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
 195 200 205
 Thr Arg Gln
 210

<210> 47
 <211> 201
 <212> PRT
 <213> homo sapiens

<400> 47
 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 1 5 10 15
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 20 25 30
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 35 40 45
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 50 55 60
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
 65 70 75 80
 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 85 90 95
 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 100 105 110
 Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
 115 120 125
 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
 130 135 140
 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 145 150 155 160
 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 165 170 175
 Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
 180 185 190
 Glu Cys Val Glu Val Gln Gly Glu Ala
 195 200

<210> 48
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 48
 His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1 5 10 15
 Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
 20 25 30
 Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
 35 40 45
 Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
 50 55 60
 Asn Leu Thr Met
 65

<210> 49
 <211> 26
 <212> PRT
 <213> mus musculus

<400> 49
 Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1 5 10 15

Ser Ala Gly Gly Pro Pro Val Thr Lys Met
 20 25

<210> 50
 <211> 28
 <212> PRT
 <213> mus musculus

<400> 50
 Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp
 1 5 10 15
 Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met
 20 25

<210> 51
 <211> 40
 <212> PRT
 <213> Mus musculus

<400> 51
 Leu Val His Pro Thr Leu Thr Pro Val Leu Ser Glu Asp Gly His Gln
 1 5 10 15
 Leu Thr Leu Glu Glu Ile Phe His Asp Leu Phe Tyr Arg Leu Glu Leu
 20 25 30
 His Val Asn His Thr Tyr Gln Met
 35 40

<210> 52
 <211> 50
 <212> PRT
 <213> Mus musculus

<400> 52
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1 5 10 15
 Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr Pro Ile Leu Ser
 20 25 30
 Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr Leu Pro Leu Val
 35 40 45
 Pro Arg
 50

<210> 53
 <211> 70
 <212> PRT
 <213> Mus musculus

<400> 53
 His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu Gly Leu Thr Pro
 1 5 10 15
 Asp Thr Glu Phe His Leu Glu Gly Lys Gln Arg Glu Tyr Glu Phe Leu
 20 25 30
 Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly Ser Ile Thr Ile Leu Thr
 35 40 45
 Pro Ile Leu Ser Lys Glu Ser Ala Pro Tyr Val Cys Arg Val Lys Thr
 50 55 60
 Leu Pro Leu Val Pro Arg
 65 70

<210> 54
 <211> 46

<212> PRT
 <213> Mus musculus

<400> 54
 Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys Val Thr Ala Val
 1 5 10 15
 Ser Ala Gly Gly Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys
 20 25 30
 Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met
 35 40 45

<210> 55
 <211> 48
 <212> PRT
 <213> mus musculus

<220>
 <221> VARIANT
 <222> 6, 11, 13,
 <223> Xaa = Any Amino Acid

<400> 55
 Thr Asp Arg Phe Ser Xaa Leu Gln His Thr Xaa Ile Xaa Pro Xaa Asp
 1 5 10 15
 Xaa Xaa Xaa Ile Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Ile
 20 25 30
 Lys Pro Pro Asp Val Thr Cys Ile Pro Lys Val Arg Ser Ile Gln Met
 35 40 45

<210> 56
 <211> 92
 <212> PRT
 <213> homo sapiens

<400> 56
 Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1 5 10 15
 Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
 20 25 30
 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met
 85 90

<210> 57
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 57
 Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp
 1 5 10 15
 Val Thr Cys Ile Ser Lys Val Arg Ser Ile Gln Met
 20 25

<210> 58
 <211> 40
 <212> PRT

<213> Homo sapiens

<400> 58
 Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly His Arg
 1 5 10 15
 Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu Glu Leu
 20 25 30
 Gln Val Asn Arg Thr Tyr Gln Met
 35 40

<210> 59

<211> 25

<212> PRT

<213> Homo sapiens

<400> 59

His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
 1 5 10 15
 Asp Thr Glu Phe Leu Gly Thr Ile Met
 20 25

<210> 60

<211> 14

<212> PRT

<213> Homo sapiens

<400> 60

Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr Met
 1 5 10

<210> 61

<211> 12

<212> PRT

<213> Homo sapiens

<400> 61

Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr
 1 5 10

<210> 62

<211> 212

<212> PRT

<213> Artificial Sequence

<220>

<223> A murine IL-22RA soluble receptor with cleavage
 site (Leu Val Pro Arg) remaining on C-Terminus

<400> 62

His Thr Thr Val Asp Thr Ser Gly Leu Leu Gln His Val Lys Phe Gln
 1 5 10 15
 Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Gly Gly Pro Ala Ser
 20 25 30
 Thr Ser Asp Thr Val Tyr Ser Val Glu Tyr Lys Lys Tyr Gly Glu Arg
 35 40 45
 Lys Trp Leu Ala Lys Ala Gly Cys Gln Arg Ile Thr Gln Lys Phe Cys
 50 55 60
 Asn Leu Thr Met Glu Thr Arg Asn His Thr Glu Phe Tyr Tyr Ala Lys
 65 70 75 80
 Val Thr Ala Val Ser Ala Gly Gly Pro Pro Val Thr Lys Met Thr Asp
 85 90 95
 Arg Phe Ser Ser Leu Gln His Thr Thr Ile Lys Pro Pro Asp Val Thr

